

## LISTE DE SEQUENCES

&lt;110&gt; Centre National de la Recherche Scientifique

LAP20 Rec'd PCT/PTO 20 JAN 2006

&lt;120&gt; Peptide inhibiteur de la traduction des protéines et utilisation pour le contrôle de la traduction des protéines

&lt;130&gt; P290-FR

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 16

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Xenopus laevis

&lt;400&gt; 1

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Thr
1				5					10					15	

Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Leu	Asn	Ala
		20						25			

&lt;210&gt; 2

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Ala
1				5					10					15	

Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Ile	Ser	Ala
		20						25			

&lt;210&gt; 3

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Xenopus laevis

&lt;400&gt; 3

Phe	Thr	Thr	Arg	Ser	Met	Ala	Gln	Met	Ala	Ile	Lys	Ser	Met	His	Gln
1				5					10					15	

Ala	Gln	Thr	Met	Glu	Gly	Cys	Ser	Ser	Pro	Ile	Val	Val	Lys	Phe	Ala
			20						25					30	

Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Thr	Gln	Gln	Leu	Gln
			35					40					45		

Gln	Gln	Met	Gln	Gln	Leu	Asn	Ala	Ala	Ser	Met	Trp	Gly	Asn	Leu	Thr
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50 55 60  
 Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr  
 65 70 75 80

Ala Ser Ser Gly

<210> 4  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met His Gln  
 1 5 10 15  
 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala  
 20 25 30  
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln  
 35 40 45  
 Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala  
 50 55 60  
 Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu  
 65 70 75 80  
 Leu Gln Gln Thr Ala Ser Ser Gly  
 85

<210> 5  
 <211> 189  
 <212> PRT  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:fusion

<400> 5  
 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala  
 1 5 10 15  
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln  
 20 25 30  
 Gln Gln Met Gln Gln Leu Asn Ala Ala Ala Met Ala Ser Asn Phe  
 35 40 45  
 Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr Gly Asp Val Thr Val  
 50 55 60  
 Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp Ile Ser Ser Asn  
 65 70 75 80  
 Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val Arg Gln Ser Ser

	85		90		95
Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val Pro Lys Val Ala	100	105	110		
Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val Ala Gly Trp Arg Ser	115	120	125		
Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala Thr Asn Ser Asp	130	135	140		
Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu Lys Asp Gly Asn	145	150	155	160	
Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile Tyr Gly Gly Gly	165	170	175		
Gly Gly Ser Gly Pro Tyr Ser Ile Val Ser Pro Lys Cys	180	185			

&lt;210&gt; 6

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Séquence artificielle

&lt;220&gt;

&lt;223&gt; Description de la séquence artificielle:fusion

&lt;400&gt; 6

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr	1	5	10	15
Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu	20	25	30	
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser	35	40	45	
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu	50	55	60	
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val	65	70	75	80
Ala Gly Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe	85	90	95	
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu	100	105	110	
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly	115	120	125	
Ile Tyr Gly Gly Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro	130	135	140	
Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala	145	150		

<210> 7  
 <211> 570  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:fusion

<400> 7  
 atggcttacc catacgatgt tccagattac gctagcgtaa agttcgcaga cactcagaaa 60  
 gacaaagaac agaagcgcat gacgcagcaa cttcagcagc aaatgcagca gctcaatgca 120  
 gcggccgccca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180  
 gacgtgactg tcgccccaaag caacttcgct aacggggtcg ctgaatggat cagctctaac 240  
 tcgcgatcac aggcttacaa agtaacctgt agcgttcgtc agagctctgc gcagaatcgc 300  
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tggatgaagag 360  
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420  
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480  
 ccgattccct cggccatcgc ggccaactcc ggcattctacg gaggtggagg tggatctggg 540  
 ccctattcta tagtgtcacc taaatgctag 570

<210> 8  
 <211> 570  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:fusion

<400> 8  
 atggcttacc catacgatgt tccagattac gctagcgtaa aatttgctga tacacagaag 60  
 gacaaagaac agaagagaat ggcccagcag ctccagcagc agatgcagca aatcagcgca 120  
 gcggccgccca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180  
 gacgtgactg tcgccccaaag caacttcgct aacggggtcg ctgaatggat cagctctaac 240  
 tcgcgatcac aggcttacaa agtaacctgt agcgttcgtc agagctctgc gcagaatcgc 300  
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tggatgaagag 360  
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420  
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480  
 ccgattccct cggccatcgc ggccaactcc ggcattctacg gaggtggagg tggatctggg 540  
 ccctattcta tagtgtcacc taaatgctag 570

<210> 9  
 <211> 489  
 <212> PRT  
 <213> Xenopus laevis

<400> 9  
 Met Asn Gly Thr Met Asp His Pro Asp His Pro Asp Pro Asp Ser Ile  
 1 5 10 15  
 Lys Met Phe Val Gly Gln Val Pro Arg Ser Trp Ser Glu Lys Glu Leu  
 20 25 30  
 Arg Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu  
 35 40 45  
 Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Ile  
 50 55 60

Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala Leu His  
 65 70 75 80  
 Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln Met Lys Pro  
 85 90 95  
 Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg Lys Leu Phe Ile  
 100 105 110  
 Gly Met Val Ser Lys Asn Cys Asn Glu Asn Asp Ile Arg Ala Met Phe  
 115 120 125  
 Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg Gly Pro Asp  
 130 135 140  
 Gly Met Ser Arg Gly Cys Ala Phe Val Thr Phe Thr Thr Arg Ser Met  
 145 150 155 160  
 Ala Gln Met Ala Ile Lys Ser Met His Gln Ala Gln Thr Met Glu Gly  
 165 170 175  
 Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln Lys Asp Lys  
 180 185 190  
 Glu Gln Lys Arg Met Thr Gln Gln Leu Gln Gln Gln Met Gln Gln Leu  
 195 200 205  
 Asn Ala Ala Ser Met Trp Gly Asn Leu Thr Gly Leu Asn Ser Leu Ala  
 210 215 220  
 Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn Leu  
 225 230 235 240  
 Asn Ser Leu Ser Gly Leu His Pro Met Gly Ala Glu Tyr Gly Thr Gly  
 245 250 255  
 Met Thr Ser Gly Leu Asn Ala Ile Gln Leu Gln Asn Leu Ala Ala Leu  
 260 265 270  
 Ala Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala  
 275 280 285  
 Leu Thr Ser Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser  
 290 295 300  
 Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly  
 305 310 315 320  
 Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser  
 325 330 335  
 Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser  
 340 345 350  
 Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly  
 355 360 365  
 Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser  
 370 375 380

Leu Leu Ser Gln Gln Gly Leu Gly Ala Ala Gly Ser Gln Lys Glu Gly  
 385 390 395 400  
 Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro Gln Glu Phe Gly  
 405 410 415  
 Asp Gln Asp Leu Leu Gln Met Phe Met Pro Phe Gly Asn Val Val Ser  
 420 425 430  
 Ser Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser Lys Cys Phe Gly  
 435 440 445  
 Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala Ala Ile Gln Ser  
 450 455 460  
 Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys Val Gln Leu Lys  
 465 470 475 480  
 Arg Ser Lys Asn Asp Ser Lys Pro Tyr  
 485

<210> 10  
 <211> 1470  
 <212> ADN  
 <213> *Xenopus laevis*

<400> 10  
 atgaatggca caatggacca cccagaccat ccggatccgg actccatcaa gatgtttgtg 60  
 ggtcagggttc ctcgaagctg gtcagagaaa gagctaagag aactcttcga gcagtacgga 120  
 gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180  
 tgctgtttta ttactttcta cacaagaaaa gctgcgttag aagcacagaa tgctttgcac 240  
 aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtga 300  
 aagaataatg ctgtggaaga ccgaaagcta tttatcggaa tggtttccaa gaattgta 360  
 gagaatgata tccgggccat gttctctccg tttggacaga tagaggaatg tcgtatcctg 420  
 cgaggccctg atggaatgag cagaggatgt gcattcgta cgtttacaac tagatccatg 480  
 gcacagatgg caatcaaadc catgcaccaa gcacaaacca tggagggctg ttcctcacca 540  
 atagtggtaa agttcgaga cactcagaaa gacaaagaac agaagcgcat gacgcagcaa 600  
 cttcagcagc aaatgcagca gctcaatgca gcctcaatgt ggggtaacct gactggactg 660  
 aacagcttgg caccocagta tttagcactc ctocagaga ccgcctcctc tgggaacctc 720  
 aactccctaa gtgggtctcca ccctatggga gctgagtagc gacttggaat gacatcaggg 780  
 cttaatgcca tacagttaca gaatttggca gcttttagcg ctgctgctag tgctgcgcag 840  
 aacaccccaa gtgcaggagc agcgctcact tcttcagca gccccctcag catcctaacc 900  
 agttccgggtt cctccccccag ttcaaataac tcatccatca acaccatggc atccctagga 960  
 gctctacaga cattggctgg gccacagct ggtctcaatg tcaattcgct tgcaggatg 1020  
 gctgcgttta atggaggcct aggcagcagt ctctccaatg gcactggcag tacgatggaa 1080  
 gcccttagtc aagcttactc tgggattcag cagtatgctg ccgctgcact tccttcactc 1140  
 tataaccaga gccttttgtc acaacagggt ttgggggctg cggggagtca gaaagaaggc 1200  
 ccagaaggag ccaacctttt tatataccac ctaccccagg agtttgggga ccaggatctc 1260  
 ctgcagatgt tcatgccatt tggaaatgtt gtgtcctcca aagttttcat cgacaaacaa 1320  
 acgaacctca gcaaagtgtt tggcttcgta agttacgaca atcccgtttc tgctcaggct 1380  
 gctatccagt ccatgaacgg ctttcagatc ggaatgaaac gcctgaaagt ccaactcaaa 1440  
 cgctccaaga atgacagcaa accctactga 1470

<210> 11  
 <211> 9  
 <212> PRT  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:peptide HA  
 <400> 11  
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
 1 5

<210> 12  
 <211> 33  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:amorce

<400> 12  
 atgctagcgt aaagttcgca gacactcaga aag 33

<210> 13  
 <211> 32  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:amorce

<400> 13  
 atgcggccgc tgcattgagc tgctgcattt gc 32

<210> 14  
 <211> 32  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:amorce

<400> 14  
 atgctagcgt aaaatttgct gatacacaga ag 32

<210> 15  
 <211> 32  
 <212> ADN  
 <213> Séquence artificielle

<220>  
 <223> Description de la séquence artificielle:amorce

<400> 15  
 atgcggccgc tgcgctgatt tgctgcatct gc 32

<210> 16  
 <211> 27  
 <212> ADN  
 <213> Séquence artificielle

<220>

<223> Description de la séquence artificielle:peptide HA

<400> 16

taccatacgt atgttccaga ttacgct

27